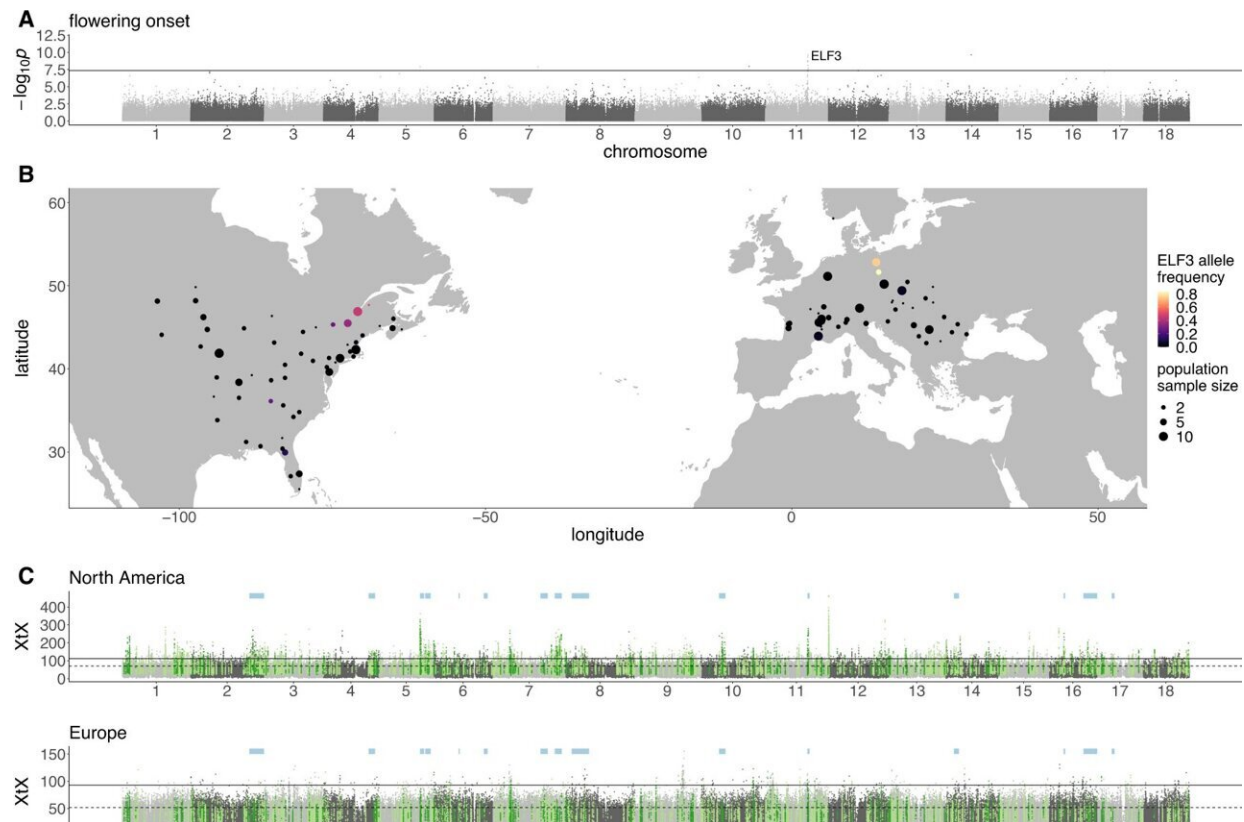


Supergenes power invasive species' success, study finds

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Signatures of climate adaptation in *Ambrosia artemisiifolia*. A GWAS $-\log_{10}p$ -value of mixed model association against genomic location for flowering onset (solid line indicates a Bonferroni-corrected p-value of 0.05). B Distribution of a strongly-associated non-synonymous SNP in ELF3 among modern *A. artemisiifolia* populations used in this study. C Genome-wide XtX scans between sampling locations within each range separately. Solid lines indicate Bonferroni-corrected significance derived from XtX p-values; dashed lines indicate the top 1% of genome-wide XtX values. Green highlights represent the top 5% of

10 kbp WZA windows for each scan that are also among the top 5% of EAA WZA windows for at least one environmental variable, with dark green indicating outlier windows shared between North America and Europe. Pale blue bars indicate the location of 15 haploblocks (putative chromosomal inversions) that overlap shared outlier windows. Credit: *Nature Communications* (2023). DOI: 10.1038/s41467-023-37303-4

Common ragweed, a pest and a major cause of hay fever, is a successful invasive species because it uses "supergenes" to adapt, an international study led by Monash University has found.

Ragweed is an invasive species on most continents including Australia and it's able to rapidly adapt to a range of environments.

Researchers from the School of Biological Sciences investigated the features of its genetic code to understand what made it so successful. The results of the study were published on March 27 in *Nature Communications*.

"One of the most exciting and unexpected findings of our study was the number and evolutionary importance of large supergenes in ragweed," said senior study author Dr. Kathryn Hodgins.

"These supergenes encompass very big chunks of the ragweed genome," she said.

"The Common ragweed is able to rapidly invade diverse environments using supergenes which affect traits, like plant size and flowering time which are critical for ragweed's survival and reproduction in different climates."

The research team sequenced the DNA of over 600 ragweed plants from North America (where ragweed is native) and Europe (where ragweed has invaded over the last 200 years).

Some of the plants they used in the study were collected from the field recently, but others were museum specimens collected as long as 190 years ago.

Working with DNA from [museum specimens](#) requires specialized equipment and expertise, so the research team collaborated on this project with ancient DNA experts from NTNU in Norway.

"This project has been so exciting because we were able to compare DNA from the past and present and directly observe the [evolutionary changes](#) that have occurred as common [ragweed](#) adapted and spread across Europe," said study first author Dr. Paul Battlay, from Monash University.

"We need to control invasive species and predict their spread to mitigate their [damaging effects](#) on our local biodiversity, economy and our health," he said.

"Identifying the DNA changes that allow [invasive species](#) to be successful gives us another weapon in our arsenal against these challenging pests."

Study first author Jonny Wilson, a Ph.D. candidate at Monash, said when he started his Ph.D. he was particularly interested in identifying structural variants such as supergenes in [invasive plants](#), which have until recently been difficult to detect due to technological constraints.

"I wasn't quite sure what to expect at first, but discovering the magnitude and importance of the role of supergenes has been well beyond what I

had hoped to find," he said.

More information: Paul Battlay et al, Large haploblocks underlie rapid adaptation in the invasive weed *Ambrosia artemisiifolia*, *Nature Communications* (2023). [DOI: 10.1038/s41467-023-37303-4](https://doi.org/10.1038/s41467-023-37303-4)

Provided by Monash University

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